AMENDMENTS TO THE CLAIMS

1. (Currently amended) A method for the fermentative production of at least one sulfur-containing fine chemical, which comprises the following steps:

a). fermentation of a coryneform bacteria culture producing the desired sulfur-containing fine chemical, the coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with ~~methionine synthase~~ methylenetetrahydrofolate reductase (metF) activity;

b) concentration of the sulfur-containing fine chemical in the medium or in the bacterial cells, and

c) isolation of the sulfur-containing fine chemical.

2. (Original) A method as claimed in claim 1, wherein the sulfur-containing fine chemical comprises L-methionine.

3. (Currently amended) A method as claimed in claim 1 ~~either of the preceding claims~~, wherein the heterologous metF-encoding nucleotide sequence is less than 100% homologous to the metF-encoding sequence from Corynebacterium glutamicum ATCC 13032.

4. (Original) A method as claimed in claim 3, wherein the metF-encoding sequence is derived from any of the following organisms:

Organism	**Strain collection**
Corynebacterium diphteriae	ATCC 14779
Streptomyces lividans	ATCC 19844
Streptomyces coelicolor	ATCC 10147
Aquifex aeolicus	DSM 6858
Burkholderia cepacia	ATCC 25416
Nitrosomonas europaea	ATCC 19718
Pseudomonas aeruginosa	ATCC 17933
Xylella fastidiosa	ATCC 35881
Pseodomonas fluorescens	ATCC 13525

Schizosaccharomyces pombe	ATCC 24969
Saccharomyces cerevisiae	ATCC 10751
Erwinia carotovora	ATCC 15713
Klebsiella pneumoniae	ATCC 700721
Salmonella typhi	ATCC 12839
Salmonella typhimurium	ATCC 15277
Escherichia coli K12	ATCC 55151
Vibrio cholerae	ATCC 39315
Haemophilus influenzae	ATCC 51907
Caulobacter crescentus	ATCC 19089
Actinobacillus actinomycetemcomitans	ATCC 33384
Neisseria meningitis	ATCC 6253
Rhodobacter capsulatus	ATCC 11166
Campylobacter jejuni	ATCC 33560
Lactococcus lactis	ATCC 7962
Prochlorococcus marinus	PCC 7118
Bacillus stearothermophilus	ATCC 12980

5. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein the metF-encoding sequence comprises a coding sequence according to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51 and 53 or a nucleotide sequence homologous thereto which codes for a protein with metF activity.

6. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein the metF-encoding sequence codes for a protein with metF activity, said protein comprising an amino acid sequence according to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52 and 54 or an amino acid sequence homologous thereto which represents a protein with metF activity.

7. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein the coding metF sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

8. (Original) A method as claimed in claim 7, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metF sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metF sequence has been integrated into the bacteria chromosome is used.

9. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein the coding metF sequence is overexpressed.

10. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of the desired sulfur-containing fine chemical has been amplified or mutated such that its activity is not influenced by metabolic metabolites.

11. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein bacteria are fermented in which at least one metabolic pathway, which reduces the production of the desired sulfur-containing fine chemical, is at least partially switched off.

12. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among

a) the lysC gene, which encodes an aspartate kinase,

b) the glyceraldehyde-3-phosphate dehydrogenase-encoding gene gap,

c) the 3-phosphoglycerate kinase-encoding gene pgk,

d) the pyruvate carboxylase-encoding gene pyc,

e) the triose phosphate isomerase-encoding gene tpi,

f) the homoserine O-acetyltransferase-encoding gene metA,

g) the cystathionine gamma-synthase-encoding gene metB,

h) the cystathionine gamma-lyase-encoding gene metC,

i) the serine hydroxymethyltransferase-encoding gene glyA,

j) the O-acetylhomoserine sulfhydrylase-encoding gene metY,

k) the vitamin B12-dependent methionine synthase-encoding gene metH,

l) the phophoserine aminotransferase-encoding gene serC,

m) the phosphoserine phosphatase-encoding gene serB,

n) the serine acetyltransferase-encoding gene cysE, and

o) the hom gene, which encodes a homoserine dehydrogenase,

is overexpressed or mutated in such a way that the activity of the corresponding proteins is influenced by metabolic metabolites to a smaller extent, if at all, compared to nonmutated proteins.

13. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among

a) the homoserine kinase-encoding gene thrB,

b) the threonine dehydratase-encoding gene ilvA,

c) the threonine synthase-encoding gene thrC,

d) the meso-diaminopimelate D-dehydrogenase-encoding gene ddh,

e) the phosphoenolpyruvate carboxykinase-encoding gene pck,

f) the glucose-6-phosphate 6-isomerase-encoding gene pgi,

g) the pyruvate oxidase-encoding gene poxB,

h) the dihydrodipicolinate synthase-encoding gene dapA,

i) the dihydrodipicolinate reductase-encoding gene dapB; and

j) the diaminopicolinate decarboxylase-encoding gene,

is attenuated by changing the rate of expression or by introducing a specific mutation.

14. (Currently amended) A method as claimed in claim 1 ~~one or more of the preceding claims~~, wherein microorganisms of the species Corynebacterium glutamicum are used.

15. (Original) A method for producing an L-methionine-containing animal feed additive from fermentation broths, which comprises the following steps:

a) culturing and fermentation of an L-methionine-producing microorganism in a fermentation medium;

b) removal of water from the L-methionine-containing fermentation broth;

c) removal of from 0 to 100% by weight of the biomass formed during fermentation; and

d) drying of the fermentation broth obtained according to b) and/or c), in order to obtain the animal feed additive in the desired powder or granule form.

16. (Currently amended) A method as claimed in claim 15, wherein the microorganisms ~~according to the definition in any of claims 1 to 14 are used~~ are coryneform bacteria expressing at least one nucleotide sequence which codes for a protein with metF activity.